IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 076518-0150

re patent application of

JEFFERSON, RICHARD *et al.*

Serial No. 09/936,759

Filed: September 17, 2000

For: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND USES THEREOF

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1.   the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2.   the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
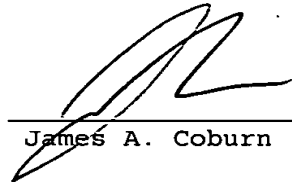
3.   all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

April 17, 2002
Date

James A. Coburn

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Portsmouth, N.H.
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     MAYER, JORGE E.

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Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro Ala Tyr Leu Lys Asp
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Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr His Lys Ala Ile Val
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Tyr Val Asn Gly Glu Leu Val Val Glu His Lys Gly Gly Phe Leu Pro
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Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly Leu His Arg Pro Val
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Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu Asp Ile Ser Val Val
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Gln Ile Val Ala Gln Gly Leu Gly Ala Thr Gly Ile Phe Glu Leu Asp
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Phe Asp Ala Gly Glu Arg Pro Lys Glu Leu Tyr Ser Glu Glu Ala Ile
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Asn Gly Glu Thr Ser Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu
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Gly Val His Leu Asn Phe Met Ala Thr Thr Gly Leu Gly Glu Gly Ser
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Asp Val Leu Arg Glu Leu Val Ser Arg Asp Lys Asn His Pro Ser Val
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Val Met Trp Ser Ile Ala Asn Glu Ala Ala Thr Glu Glu Glu Gly Ala
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Tyr Glu Tyr Phe Lys Pro Leu Gly Gly Ala Ala Lys Glu Leu Asp Pro
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Thr Asp Lys Val Ala Glu Leu Ile Asp Val Ile Ala Leu Asn Arg Tyr
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Ala Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Val Met Arg Val
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Asp Thr Trp Thr Xaa Ser Leu Leu Thr Glu Leu Ser Arg Leu Val Val
            35                  40                  45

Leu Ser Trp Thr Thr His Xaa Leu Thr Gly Glu Xaa Pro Ala Ile Ser
      50                  55                  60

Ile Leu Trp Pro Asn Ser Glu Leu Thr Val Ser Xaa Leu Tyr Xaa Gly
 65                  70                  75                  80

Ser Leu Xaa Ser Ser Ser Xaa Leu Cys Ser Ser Leu Thr Xaa His Val
                85                  90                  95

Val Ile Cys Gln Xaa Val Thr Leu Xaa Val Asp His Thr Gly Leu Ile
            100                 105                 110

Xaa Xaa Phe Glu Phe Met Ser Thr Thr Cys Cys Xaa Xaa Asp Glu Leu
            115                 120                 125

Val Thr Gly Thr Leu Ala Xaa Ile Leu Tyr His Xaa Ile Leu Pro His
      130                 135                 140

Gly Leu Tyr Arg Lys Arg His Glu Xaa Gly Leu Gly Lys Xaa Asn Phe
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Tyr Xaa Leu His Phe Ala Phe Phe Xaa Tyr Ala Xaa Leu Xaa Arg Thr
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Val Xaa Met Tyr Xaa Asn Leu Val Arg Xaa Gln Asp Ile Xaa Val Val
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Thr Xaa Xaa His Xaa Xaa Xaa Xaa Thr Val Glu Gln Cys Val Xaa Xaa
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Asn Xaa Lys Ile Xaa Ser Val Lys Ile Thr Ile Leu Asp Glu Asn Asp
210   215   220

His Ala Ile Xaa Glu Ser Glu Gly Ala Lys Gly Asn Val Thr Ile Gln
225   230   235   240

Asn Pro Ile Leu Trp Gln Pro Leu His Ala Tyr Leu Tyr Asn Met Lys
         245   250   255

Val Glu Leu Leu Asn Asp Asn Glu Cys Val Asp Val Tyr Thr Glu Arg
        260   265   270

Phe Gly Ile Arg Ser Val Glu Val Lys Asp Gly Gln Phe Leu Ile Asn
    275   280   285

Asp Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys His Glu Asp Thr Tyr
   290   295   300

Xaa Asn Gly Arg Gly Leu Asn Glu Ser Ala Asn Val Met Asp Ile Asn
305   310   315   320

Leu Met Lys Trp Ile Gly Ala Asn Ser Phe Arg Thr Ser His Tyr Pro
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Tyr Ser Glu Glu Met Met Arg Leu Ala Asp Glu Gln Gly Ile Val Val
       340   345   350

Ile Asp Glu Thr Thr Xaa Val Gly Ile His Leu Asn Phe Met Xaa Thr
    355   360   365

Leu Gly Gly Ser Xaa Ala His Asp Thr Trp Xaa Glu Phe Asp Thr Leu
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Glu Phe His Lys Glu Val Ile Xaa Asp Leu Ile Xaa Arg Asp Lys Asn
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Ile Glu Val Ser Glu Glu Ala Val Gly Gln Glu Met Thr Ile Lys Leu
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Gly Glu Glu Glu Lys Lys Ile Arg Thr Ser Asn Arg Phe Val Glu Gly
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Glu Phe Ile Leu Glu Asn Ala Arg Phe Trp Ser Leu Glu Asp Pro Tyr
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Leu Tyr Pro Leu Lys Val Glu Leu Glu Lys Asp Glu Tyr Thr Leu Asp
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Ile Gly Ile Arg Thr Ile Ser Trp Asp Glu Lys Arg Leu Tyr Leu Asn
            260   265   270

Gly Lys Pro Val Phe Leu Lys Gly Phe Gly Lys His Glu Glu Phe Pro
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Val Leu Gly Gln Gly Thr Phe Tyr Pro Leu Met Ile Lys Asp Phe Asn
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Leu Leu Lys Trp Ile Asn Ala Asn Ser Phe Arg Thr Ser His Tyr Pro
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Tyr Ser Glu Glu Trp Leu Asp Leu Ala Asp Arg Leu Gly Ile Leu Val
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Ile Asp Glu Ala Pro His Val Gly Ile Thr Arg Tyr His Tyr Asn Pro
            340   345   350

Glu Thr Gln Lys Ile Ala Glu Asp Asn Ile Arg Arg Met Ile Asp Arg
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His Lys Asn His Pro Ser Val Ile Met Trp Ser Val Ala Asn Glu Pro
    370   375   380

Glu Ser Asn His Pro Asp Ala Glu Gly Phe Phe Lys Ala Leu Tyr Glu
385   390   395   400

Thr Ala Asn Glu Met Asp Arg Thr Arg Pro Val Val Met Val Ser Met
                405   410   415

Met Asp Ala Pro Asp Glu Arg Thr Arg Asp Val Ala Leu Lys Tyr Phe
            420   425   430

Asp Ile Val Cys Val Asn Arg Tyr Tyr Gly Trp Tyr Ile Tyr Gln Gly
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Arg Ile Glu Glu Gly Leu Gln Ala Leu Glu Lys Asp Ile Glu Glu Leu
    450   455   460

Tyr Ala Arg His Arg Lys Pro Ile Phe Val Thr Glu Phe Gly Ala Asp
465   470   475   480

Ala Ile Ala Gly Ile His Tyr Asp Pro Pro Gln Met Phe Ser Glu Glu
                485   490   495

Tyr Gln Ala Glu Leu Val Glu Lys Thr Ile Arg Leu Leu Leu Lys Lys
            500   505   510

Asp Tyr Ile Ile Gly Thr His Val Trp Ala Phe Ala Asp Phe Lys Thr
        515   520   525

Pro Gln Asn Val Arg Arg Pro Ile Leu Asn His Lys Gly Val Phe Thr
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Arg Asp Arg Gln Pro Lys Leu Val Ala His Val Leu Arg Arg Leu Trp
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Ser Glu Val

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ggg gtc tgg aat ttt aaa tta gat tac ggc aaa gga ctg gaa gaa aag   96
Gly Val Trp Asn Phe Lys Leu Asp Tyr Gly Lys Gly Leu Glu Glu Lys
                20   25   30

tgg tat gaa tca aaa ctg aca gat acc ata tca atg gct gta cct tcc   144
Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser Met Ala Val Pro Ser
            35   40   45

tcc tat aat gat atc ggt gtt acg aag gaa att cga aac cat atc ggc   192
Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile Arg Asn His Ile Gly
        50   55   60

tat gta tgg tac gag cgt gaa ttt acc gtt cct gct tat tta aaa gat   240
Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro Ala Tyr Leu Lys Asp
65   70   75   80

cag cgc atc gtc ctg cgt ttt ggt tca gca aca cat aag gct att gta   288
Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr His Lys Ala Ile Val
                85   90   95

tac gtt aac gga gaa cta gta gtt gaa cac aaa ggc ggc ttc tta ccg   336
Tyr Val Asn Gly Glu Leu Val Val Glu His Lys Gly Gly Phe Leu Pro
            100   105   110

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ttt gag gca gaa ata aac aac agc tta aga gac gga atg aat cgt gta    384
Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp Gly Met Asn Arg Val
        115                 120                 125

aca gta gcg gtt gat aat att tta gat gat tct acg ctc cca gtt ggg    432
Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser Thr Leu Pro Val Gly
        130                 135                 140

cta tat agt gaa aga cat gaa gaa ggt ttg gga aaa gtg att cgt aat    480
Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly Lys Val Ile Arg Asn
145                 150                 155                 160

aaa cct aat ttt gac ttc ttt aac tat gca ggc tta cat cgt cct gta    528
Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly Leu His Arg Pro Val
                165                 170                 175

aaa att tat aca acc cct ttt acc tat gtt gag gat ata tcg gtt gta    576
Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu Asp Ile Ser Val Val
                180                 185                 190

acc gat ttt aac ggt cca acg gga aca gtt acg tat aca gtt gat ttt    624
Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr Tyr Thr Val Asp Phe
                195                 200                 205

cag ggt aag gca gaa acc gta aag gtt agt gta gtt gat gaa gaa ggg    672
Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val Val Asp Glu Glu Gly
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aaa gtt gtt gct tca act gaa ggc ctc tct ggt aat gtt gag att cct    720
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225                 230                 235                 240

aac gtt atc ctt tgg gaa cct tta aat acc tat ctc tat caa att aaa    768
Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr Leu Tyr Gln Ile Lys
                245                 250                 255

gtt gag tta gta aat gat ggt cta act att gat gta tac gaa gag cca    816
Val Glu Leu Val Asn Asp Gly Leu Thr Ile Asp Val Tyr Glu Glu Pro
                260                 265                 270

ttt gga gtt cga acc gtt gaa gta aac gac ggg aaa ttc ctc att aat    864
Phe Gly Val Arg Thr Val Glu Val Asn Asp Gly Lys Phe Leu Ile Asn
        275                 280                 285

aac aaa cca ttt tat ttt aaa ggg ttc gga aaa cac gag gat act cca    912
Asn Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys His Glu Asp Thr Pro
        290                 295                 300

ata aat gga aga ggc ttt aat gaa gca tca aat gta atg gat ttt aat    960
Ile Asn Gly Arg Gly Phe Asn Glu Ala Ser Asn Val Met Asp Phe Asn
305                 310                 315                 320

att ttg aaa tgg atc ggt gcg aat tcc ttt cgg acg gcg cac tat cct   1008
Ile Leu Lys Trp Ile Gly Ala Asn Ser Phe Arg Thr Ala His Tyr Pro
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tat tct gaa gaa ctg atg cgg ctc gca gat cgt gaa ggg tta gtc gtc    1056
Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg Glu Gly Leu Val Val
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ata gat gaa acc cca gca gtt ggt gtt cat ttg aac ttt atg gca acg    1104
Ile Asp Glu Thr Pro Ala Val Gly Val His Leu Asn Phe Met Ala Thr
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act ggt ttg ggc gaa ggt tca gag aga gtg agt act tgg gaa aaa atc    1152
Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser Thr Trp Glu Lys Ile
            370             375             380

cgg acc ttt gaa cat cat caa gat gta ctg aga gag ctg gtt tct cgt    1200
Arg Thr Phe Glu His His Gln Asp Val Leu Arg Glu Leu Val Ser Arg
385             390             395             400

gat aaa aac cac ccc tct gtt gtc atg tgg tcg att gca aat gaa gcg    1248
Asp Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Ala
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gct acg gaa gaa gaa ggc gct tat gaa tac ttt aag cca tta gtt gaa    1296
Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe Lys Pro Leu Val Glu
            420             425             430

tta acg aaa gaa tta gat cca caa aaa cgc cca gtt acc att gtt ttg    1344
Leu Thr Lys Glu Leu Asp Pro Gln Lys Arg Pro Val Thr Ile Val Leu
            435             440             445

ttc gta atg gcg aca cca gaa aca gat aaa gtg gcg gag tta att gat    1392
Phe Val Met Ala Thr Pro Glu Thr Asp Lys Val Ala Glu Leu Ile Asp
            450             455             460

gtg att gca ttg aat cga tac aac ggc tgg tat ttt gat ggg ggt gat    1440
Val Ile Ala Leu Asn Arg Tyr Asn Gly Trp Tyr Phe Asp Gly Gly Asp
465             470             475             480

ctt gaa gcc gcg aaa gtc cac ctt cgt cag gaa ttt cat gcg tgg aat    1488
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aaa cgc tgt cca gga aaa cct ata atg ata aca gag tat ggg gct gat    1536
Lys Arg Cys Pro Gly Lys Pro Ile Met Ile Thr Glu Tyr Gly Ala Asp
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acc gta gct ggt ttt cat gat att gat ccg gtt atg ttt aca gaa gag    1584
Thr Val Ala Gly Phe His Asp Ile Asp Pro Val Met Phe Thr Glu Glu
            515             520             525

tat cag gtt gaa tat tac caa gca aat cat gta gta ttt gat gaa ttt    1632
Tyr Gln Val Glu Tyr Tyr Gln Ala Asn His Val Val Phe Asp Glu Phe
            530             535             540

gag aac ttt gtt ggc gag cag gcc tgg aat ttt gca gac ttt gct aca    1680
Glu Asn Phe Val Gly Glu Gln Ala Trp Asn Phe Ala Asp Phe Ala Thr
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agc cag ggt gtc atg cgt gtt caa ggt aac aaa aaa ggt gtt ttc aca   1728
Ser Gln Gly Val Met Arg Val Gln Gly Asn Lys Lys Gly Val Phe Thr
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cgc gac cgc aaa cca aaa tta gca gca cat gtt ttc cgc gaa cgt tgg   1776
Arg Asp Arg Lys Pro Lys Leu Ala Ala His Val Phe Arg Glu Arg Trp
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Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser Met Ala Val Pro Ser
                35                  40                  45

Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile Arg Asn His Ile Gly
     50                  55                  60

Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro Ala Tyr Leu Lys Asp
 65                  70                  75                  80

Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr His Lys Ala Ile Val
                85                  90                  95

Tyr Val Asn Gly Glu Leu Val Val Glu His Lys Gly Gly Phe Leu Pro
                100                 105                 110

Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp Gly Met Asn Arg Val
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Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser Thr Leu Pro Val Gly
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Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly Lys Val Ile Arg Asn
145                 150                 155                 160

Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly Leu His Arg Pro Val
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Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu Asp Ile Ser Val Val
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Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr Tyr Thr Val Asp Phe
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Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val Val Asp Glu Glu Gly
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Lys Val Val Ala Ser Thr Glu Gly Leu Ser Gly Asn Val Glu Ile Pro
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Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr Leu Tyr Gln Ile Lys
                245             250                 255

Val Glu Leu Val Asn Asp Gly Leu Thr Ile Asp Val Tyr Glu Glu Pro
                260             265             270

Phe Gly Val Arg Thr Val Glu Val Asn Asp Gly Lys Phe Leu Ile Asn
        275             280             285

Asn Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys His Glu Asp Thr Pro
    290             295             300

Ile Asn Gly Arg Gly Phe Asn Glu Ala Ser Asn Val Met Asp Phe Asn
305             310             315             320

Ile Leu Lys Trp Ile Gly Ala Asn Ser Phe Arg Thr Ala His Tyr Pro
                325             330             335

Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg Glu Gly Leu Val Val
            340             345             350

Ile Asp Glu Thr Pro Ala Val Gly Val His Leu Asn Phe Met Ala Thr
            355             360             365

Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser Thr Trp Glu Lys Ile
    370             375             380

Arg Thr Phe Glu His His Gln Asp Val Leu Arg Glu Leu Val Ser Arg
385             390             395             400

Asp Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Ala
            405             410             415

Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe Lys Pro Leu Val Glu
            420             425             430

Leu Thr Lys Glu Leu Asp Pro Gln Lys Arg Pro Val Thr Ile Val Leu
            435             440             445

Phe Val Met Ala Thr Pro Glu Thr Asp Lys Val Ala Glu Leu Ile Asp
    450             455             460

Val Ile Ala Leu Asn Arg Tyr Asn Gly Trp Tyr Phe Asp Gly Gly Asp
465             470             475             480

Leu Glu Ala Ala Lys Val His Leu Arg Gln Glu Phe His Ala Trp Asn
            485             490             495

Lys Arg Cys Pro Gly Lys Pro Ile Met Ile Thr Glu Tyr Gly Ala Asp
        500             505             510
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Thr Val Ala Gly Phe His Asp Ile Asp Pro Val Met Phe Thr Glu Glu
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Tyr Gln Val Glu Tyr Tyr Gln Ala Asn His Val Val Phe Asp Glu Phe
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Glu Asn Phe Val Gly Glu Gln Ala Trp Asn Phe Ala Asp Phe Ala Thr
545   550   555   560

Ser Gln Gly Val Met Arg Val Gln Gly Asn Lys Lys Gly Val Phe Thr
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Arg Asp Arg Lys Pro Lys Leu Ala Ala His Val Phe Arg Glu Arg Trp
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<221> modified_base
<222> (1535)..(1536)
<223> a, c, t, g, other or unknown

<220>
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<222> (1551)..(1552)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (1557)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (1571)..(1572)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (1593)
<223> a, c, t, g, other or unknown

<220>
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<222> (1605)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (1609)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (1688)
<223> a, c, t, g, other or unknown

<400> 12
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ttgctgaccg aactatcacg actggtcgtg ctaagttgga ccacacattn cctgacaggg 180
gaaanacccg ccatatccat cttgtggccc aacagtgagt taaccgtgtc gancttatat 240
ganggatcac tgnattcgag ctccntctta tgttcttcgc taacatanca tgtngtcata 300
tgtcaatang tgacnctggn cgtggatcac accgggctna ttgntgnatt cgaatttatg 360
tcaacaactt gttgcangnt ggatgaattg gtnacaggga ctttggccan catcctatac 420
catngcatcc ttccccatgg gctttaccga aagcgccacg aaaanggcct cggaaaagnc 480
aatttttacn ggctccactt tgcntttttc aantatgcng anctgnaccg gacggtnana 540
atgtacanga accttgtacg tcnncaagac atttaggttg tgaccgntta gcatnagcng 600
tnntaaacag tagaacaatg tgtganccnt aactaaaaaa tanacagcgt taaaatcacg 660
attctggatg aaaatgatca tgcaatancc gaaagcgaag gcgctaaagg caatgtaact 720
attcaaaatc ctatattgtg gcaaccttta catgcctatt tatacaatat gaaagtagaa 780
ttactcaacg ataatgagtg tgtagatgtt tatacagaac gtttcggtat tcgatctgtn 840
gaagtgaagg atggacagtt tttaattaat gacaaaccat tttatttcaa aggtttcggt 900
aaacatgaag atacctatta aaatggtcga ggcttaaacg aatcagccaa cgtcatggac 960
atcaacttaa tgaaatggat aggtgctaat tcatttagaa cctctcatta cccatattca 1020
gaagaaatga tgcgtttagc agatgaacaa ggtattgtag tgatagatga gacaacangt 1080
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aagaatcatg catgggtagt catgtggtna tttggcaatg agcnagggtn aaataaaggg 1260
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ttagtcgatg tggtttgtct nnnnagnnnn tanggttggt atncacaatc aggtgattta 1440
gaaggtgcta aacnagcatt agataaggag ntagncgaat ggtggaaang acaacnaaat 1500
aagccaatna tgtttacaga gtatggtgtg gatanngttg taggtttaca nncgatncct 1560
gataaaatgc nnccagaaga gtataaaatg agnttttata aaggntatna taaaattatg 1620
gataaacgat cgcagctgag tacacgagct cacccgcgga gtcgacaaga tccaagtact 1680
acccgggnat acgtaactag tgcatgctcg cgaaatattt aggccttatc gaattaat   1738
```

<210> 13
<211> 628
<212> DNA
<213> Staphylococcus hominis

<220>
<221> modified_base
<222> (7)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (20)
<223> a, c, t, g, other or unknown

<400> 13
```
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tcctcagtcg ccgcctcgtt ggcgatgctc cacatcacga cgcttggatg gttcttgtca 120
cgagacacca gttcacggag aacgtcttga tggtgctcaa acgtccgaat cttctcccag 180
gtactgacgc gctcgctgcc ttcgccgagt cccgtggtgg ccatgaagtt gaggtgcacg 240
ccaactgccg gagtctcgtc gatcacgacc agaccctcgc gatccgcaag acgcatcaac 300
tcttcagagt acggatagtg tgcggtccgg aagctgttgg cgccgatcca tttgaggata 360
ttgaaatcca tcacattgct cgcttcgtta aagccacggc cgttgatagg agtgtcctca 420
tgtttgccaa agcccttgaa gtagaacggt ttgttgttga tgaggaactt gccgtcgttg 480
acttcacggt ccgcacgccg aacggctctt catagacatc gatggtcaag tcccgtcgtt 540
caccagttcc actttgatct ggtagagata cgtgttcaag tggttcccag aggatgacat 600
tcggaatctt cacgttaccg ctcaagcc                                    628
```

```
<210> 14
<211> 1689
<212> DNA
<213> Thermotoga maritima

<220>
<221> modified_base
<222> (181)
<223> a, c, t, g, other or unknown

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caggatctgt gctacgaaga aggacccttc acctacaaaa ccaccttcta cgttccgaag 180
naactttcac aaaaacacat cagactttac tttgctgcgg tgaacacgga ctgcgaggtc 240
ttcctcaacg gagagaaagt gggagagaat cacattgaat accttccctt cgaagtagat 300
gtgacgggga aagtgaaatc cggagagaac gaactcaggg tggttgttga aacagattg 360
aaagtgggag gatttccctc gaaggttcca gacagcggca ctcacaccgt gggatttttt 420
ggaagtttc cacctgcaaa cttcgacttc ttcccctacg gtggaatcat aaggcctgtt 480
ctgatagagt tcacagacca cgcgaggata ctcgacatct gggtggacac gagtgagtct 540
gaaccggaga agaaacttgg aaaagtgaaa gtgaagatag aagtctcaga agaagcggtg 600
ggacaggaga tgacgatcaa acttggagag gaagagaaaa agattagaac atccaacaga 660
ttcgtcgaag gggagttcat cctcgaaaac gccaggttct ggagcctcga agatccatat 720
ctttatcctc tcaaggtgga acttgaaaaa gacgagtaca ctctggacat cggaatcaga 780
acgatcagct gggacgagaa gaggctctat ctgaacggga aacctgtctt tttgaagggc 840
tttggaaagc acgaggaatt ccccgttctg gggcagggca ccttttatcc attgatgata 900
aaagacttca accttctgaa gtggatcaac gcgaattctt tcaggacctc tcactatcct 960
tacagtgaag agtggctgga tcttgccgac agactcggaa tccttgtgat agacgaagcc 1020
ccgcacgttg gtatcacaag gtaccactac aatcccgaga ctcagaagat agcagaagac 1080
aacataagaa gaatgatcga cagacacaag aaccatccca gtgtgatcat gtggagtgtg 1140
gcgaacgaac cagagtccaa ccatccagac gcggagggtt tcttcaaagc cctttatgag 1200
actgccaatg aaatggatcg aacacgcccc gttgtcatgg tgagcatgat ggacgcacca 1260
gacgagagaa caagagacgt ggcgctgaag tacttcgaca tcgtctgtgt gaacaggtac 1320
tacggctggt acatctatca gggaaggata gaagaaggac ttcaagctct ggaaaaagac 1380
atagaagagc tctatgcaag gcacagaaag cccatctttg tcacagaatt cggtgcggac 1440
gcgatagctg gcatccacta cgatccacct caaatgttct ccgaagagta ccaagcagag 1500
ctcgttgaaa agacgatcag gctcctttg aaaaaagact acatcatcgg aacacacgtg 1560
tgggcctttg cagattttaa gactcctcag aatgtgagaa gacccattct caaccacaag 1620
ggtgttttca aagagacag acaacccaaa ctcgttgctc atgtactgag aagactgtgg 1680
agtgaggtt                                                         1689


<210> 15
<211> 602
<212> PRT
<213> Staphylococcus sp.

<400> 15
Met Leu Tyr Pro Ile Asn Thr Glu Thr Arg Gly Val Phe Asp Leu Asn
1               5                   10                  15

Gly Val Trp Asn Phe Lys Leu Asp Tyr Gly Lys Gly Leu Glu Glu Lys
            20                  25                  30

Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser Met Ala Val Pro Ser
        35                  40                  45
```

```
Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile Arg Asn His Ile Gly
    50                  55                  60

Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro Ala Tyr Leu Lys Asp
65                  70                  75                      80

Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr His Lys Ala Ile Val
                85                  90                  95

Tyr Val Asn Gly Glu Leu Val Val Glu His Lys Gly Gly Phe Leu Pro
            100                 105                 110

Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp Gly Met Asn Arg Val
        115                 120                 125

Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser Thr Leu Pro Val Gly
    130                 135                 140

Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly Lys Val Ile Arg Asn
145                 150                 155                 160

Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly Leu His Arg Pro Val
                165                 170                 175

Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu Asp Ile Ser Val Val
            180                 185                 190

Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr Tyr Thr Val Asp Phe
        195                 200                 205

Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val Val Asp Glu Glu Gly
    210                 215                 220

Lys Val Val Ala Ser Thr Glu Gly Leu Ser Gly Asn Val Glu Ile Pro
225                 230                 235                 240

Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr Leu Tyr Gln Ile Lys
                245                 250                 255

Val Glu Leu Val Asn Asp Gly Leu Thr Ile Asp Val Tyr Glu Glu Pro
            260                 265                 270

Phe Gly Val Arg Thr Val Glu Val Asn Asp Gly Lys Phe Leu Ile Asn
        275                 280                 285

Asn Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys His Glu Asp Thr Pro
    290                 295                 300

Ile Asn Gly Arg Gly Phe Asn Glu Ala Ser Asn Val Met Asp Phe Asn
305                 310                 315                 320

Ile Leu Lys Trp Ile Gly Ala Asn Ser Phe Arg Thr Ala His Tyr Pro
                325                 330                 335

Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg Glu Gly Leu Val Val
        340                 345                 350
```

```
Ile Asp Glu Thr Pro Ala Val Gly Val His Leu Asn Phe Met Ala Thr
    355                 360                 365

Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser Thr Trp Glu Lys Ile
    370                 375                 380

Arg Thr Phe Glu His His Gln Asp Val Leu Arg Glu Leu Val Ser Arg
385                 390                 395                 400

Asp Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Ala
                405                 410                 415

Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe Lys Pro Leu Val Glu
                420                 425                 430

Leu Thr Lys Glu Leu Asp Pro Gln Lys Arg Pro Val Thr Ile Val Leu
        435                 440                 445

Phe Val Met Ala Thr Pro Glu Thr Asp Lys Val Ala Glu Leu Ile Asp
    450                 455                 460

Val Ile Ala Leu Asn Arg Tyr Asn Gly Trp Tyr Phe Asp Gly Gly Asp
465                 470                 475                 480

Leu Glu Ala Ala Lys Val His Leu Arg Gln Glu Phe His Ala Trp Asn
                485                 490                 495

Lys Arg Cys Pro Gly Lys Pro Ile Met Ile Thr Glu Tyr Gly Ala Asp
                500                 505                 510

Thr Val Ala Gly Phe His Asp Ile Asp Pro Val Met Phe Thr Glu Glu
        515                 520                 525

Tyr Gln Val Glu Tyr Tyr Gln Ala Asn His Val Val Phe Asp Glu Phe
    530                 535                 540

Glu Asn Phe Val Gly Glu Gln Ala Trp Asn Phe Ala Asp Phe Ala Thr
545                 550                 555                 560

Ser Gln Gly Val Met Arg Val Gln Gly Asn Lys Lys Gly Val Phe Thr
                565                 570                 575

Arg Asp Arg Lys Pro Lys Leu Ala Ala His Val Phe Arg Glu Arg Trp
            580                 585                 590

Thr Asn Ile Pro Asp Phe Gly Tyr Lys Asn
        595                 600


<210> 16
<211> 613
<212> PRT
<213> Homo sapiens

<400> 16
Leu Gly Leu Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser Arg
 1               5                   10                  15
```

Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe Ser
        20   25   30

Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro Leu
        35   40   45

Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro Ser Ser Phe Asn
    50   55   60

Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val Trp
65   70   75   80

Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu Arg
            85   90   95

Thr Arg Val Val Leu Arg Ile Gly Ser Ala His Ser Tyr Ala Ile Val
            100   105   110

Trp Val Asn Gly Val Asp Thr Leu Glu His Glu Gly Gly Tyr Leu Pro
        115   120   125

Phe Glu Ala Asp Ile Ser Asn Leu Val Gln Val Gly Pro Leu Pro Ser
    130   135   140

Arg Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu Thr Pro Thr Thr
145   150   155   160

Leu Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr Ser Lys Tyr Pro
            165   170   175

Lys Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr Ala
            180   185   190

Gly Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr Ile
        195   200   205

Asp Asp Ile Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu Val
    210   215   220

Asn Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu Val
225   230   235   240

Arg Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr
            245   250   255

Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr Leu
            260   265   270

Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln Leu Thr
        275   280   285

Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr Leu Pro Val
    290   295   300

Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe Leu Ile Asn Gly
305   310   315   320

Lys Pro Phe Tyr Phe His Gly Val Asn Lys His Glu Asp Ala Asp Ile

```
                325                    330                    335

Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys Asp Phe Asn Leu
            340                 345                 350

Leu Arg Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser His Tyr Pro Tyr
            355                 360                 365

Ala Glu Glu Val Met Gln Met Cys Asp Arg Tyr Gly Ile Val Val Ile
    370                 375                 380

Asp Glu Cys Pro Gly Val Gly Leu Ala Leu Pro Gln Phe Phe Asn Asn
385                 390                 395                 400

Val Ser Leu His His His Met Gln Val Met Glu Glu Val Val Arg Arg
            405                 410                 415

Asp Lys Asn His Pro Ala Val Val Met Trp Ser Val Ala Asn Glu Pro
            420                 425                 430

Ala Ser His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala
            435                 440                 445

His Thr Lys Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn
    450                 455                 460

Ser Asn Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys
465                 470                 475                 480

Leu Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu
                485                 490                 495

Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys Tyr
            500                 505                 510

Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile Ala Gly
    515                 520                 525

Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu Tyr Gln Lys Ser
    530                 535                 540

Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys Arg Arg Lys Tyr
545                 550                 555                 560

Val Val Gly Glu Leu Ile Trp Asn Phe Ala Asp Phe Met Thr Glu Gln
            565                 570                 575

Ser Pro Thr Arg Val Leu Gly Asn Lys Lys Gly Ile Phe Thr Arg Gln
            580                 585                 590

Arg Gln Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu Arg Tyr Trp Lys
            595                 600                 605

Ile Ala Asn Glu Thr
    610
```

<210> 17

<211> 603
<212> PRT
<213> Escherichia coli

<400> 17

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Met Leu Arg Pro Val Glu Thr Pro Thr Arg Glu Ile Lys Lys Leu Asp
1               5                   10                  15

Gly Leu Trp Ala Phe Ser Leu Asp Arg Glu Asn Cys Gly Ile Asp Gln
            20                  25                  30

Arg Trp Trp Glu Ser Ala Leu Gln Glu Ser Arg Ala Ile Ala Val Pro
            35                  40                  45

Gly Ser Phe Asn Asp Gln Phe Ala Asp Ala Asp Ile Arg Asn Tyr Ala
    50                  55                  60

Gly Asn Val Trp Tyr Gln Arg Glu Val Phe Ile Pro Lys Gly Trp Ala
65                  70                  75                  80

Gly Gln Arg Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr Gly Lys
                85                  90                  95

Val Trp Val Asn Asn Gln Glu Val Met Glu His Gln Gly Gly Tyr Thr
                100                 105                 110

Pro Phe Glu Ala Asp Val Thr Pro Tyr Val Ile Ala Gly Lys Ser Val
        115                 120                 125

Arg Ile Thr Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr Ile Pro
    130                 135                 140

Pro Gly Met Val Ile Thr Asp Glu Asn Gly Lys Lys Lys Gln Ser Tyr
145                 150                 155                 160

Phe His Asp Phe Phe Asn Tyr Ala Gly Ile His Arg Ser Val Met Leu
                165                 170                 175

Tyr Thr Thr Pro Asn Thr Trp Val Asp Asp Ile Thr Val Val Thr His
                180                 185                 190

Val Ala Gln Asp Cys Asn His Ala Ser Val Asp Trp Gln Val Val Ala
        195                 200                 205

Asn Gly Asp Val Ser Val Glu Leu Arg Asp Ala Asp Gln Gln Val Val
    210                 215                 220

Ala Thr Gly Gln Gly Thr Ser Gly Thr Leu Gln Val Val Asn Pro His
225                 230                 235                 240

Leu Trp Gln Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Cys Val Thr Ala
                245                 250                 255

Lys Ser Gln Thr Glu Cys Asp Ile Tyr Pro Leu Arg Val Gly Ile Arg
                260                 265                 270

Ser Val Ala Val Lys Gly Glu Gln Phe Leu Ile Asn His Lys Pro Phe
        275                 280                 285
```

```
Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly Lys
    290             295         300
```

```
Gly Phe Asp Asn Val Leu Met Val His Asp His Ala Leu Met Asp Trp
305             310         315                 320
```

```
Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu
            325         330                 335
```

```
Met Leu Asp Trp Ala Asp Glu His Gly Ile Val Val Ile Asp Glu Thr
        340             345             350
```

```
Ala Ala Val Gly Phe Asn Leu Ser Leu Gly Ile Gly Phe Glu Ala Gly
        355             360             365
```

```
Asn Lys Pro Lys Glu Leu Tyr Ser Glu Glu Ala Val Asn Gly Glu Thr
    370             375             380
```

```
Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp Lys
385             390             395             400
```

```
Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp Thr
            405             410             415
```

```
Arg Pro Gln Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Glu Ala Thr
        420             425             430
```

```
Arg Lys Leu Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met Phe
    435             440             445
```

```
Cys Asp Ala His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val Leu Cys
    450             455             460
```

```
Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu Thr
465             470             475             480
```

```
Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu
            485             490             495
```

```
His Gln Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala Gly
            500             505             510
```

```
Leu His Ser Met Tyr Thr Asp Met Trp Ser Glu Glu Tyr Gln Cys Ala
        515             520             525
```

```
Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val Val
    530             535             540
```

```
Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Ile
545             550             555             560
```

```
Leu Arg Val Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg Lys
            565             570             575
```

```
Pro Lys Ser Ala Ala Phe Leu Leu Gln Lys Arg Trp Thr Gly Met Asn
        580             585             590
```

Phe Gly Glu Lys Pro Gln Gln Gly Gly Lys Gln
        595   600

<210> 18
<211> 607
<212> PRT
<213> Staphylococcus sp.

<400> 18
Met Val Asp Leu Thr Ser Leu Tyr Pro Ile Asn Thr Glu Thr Arg Gly
 1   5   10   15

Val Phe Asp Leu Asn Gly Val Trp Asn Phe Lys Leu Asp Tyr Gly Lys
            20   25   30

Gly Leu Glu Glu Lys Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser
        35   40   45

Met Ala Val Pro Ser Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile
    50   55   60

Arg Asn His Ile Gly Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro
65   70   75   80

Ala Tyr Leu Lys Asp Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr
            85   90   95

His Lys Ala Ile Val Tyr Val Asn Gly Glu Leu Val Val Glu His Lys
            100   105   110

Gly Gly Phe Leu Pro Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp
        115   120   125

Gly Met Asn Arg Val Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser
    130   135   140

Thr Leu Pro Val Gly Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly
145   150   155   160

Lys Val Ile Arg Asn Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly
            165   170   175

Leu His Arg Pro Val Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu
            180   185   190

Asp Ile Ser Val Val Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr
        195   200   205

Tyr Thr Val Asp Phe Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val
    210   215   220

Val Asp Glu Glu Gly Lys Val Val Ala Ser Thr Glu Gly Leu Ser Gly
225   230   235   240

Asn Val Glu Ile Pro Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr
            245   250   255

Leu Tyr Gln Ile Lys Val Glu Leu Val Asn Asp Gly Leu Thr Ile Asp
            260   265   270

Val Tyr Glu Glu Pro Phe Gly Val Arg Thr Val Glu Val Asn Asp Gly
            275   280   285

Lys Phe Leu Ile Asn Asn Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys
        290   295   300

His Glu Asp Thr Pro Ile Asn Gly Arg Gly Phe Asn Glu Ala Ser Asn
305   310   315   320

Val Met Asp Phe Asn Ile Leu Lys Trp Ile Gly Ala Asn Ser Phe Arg
                325   330   335

Thr Ala His Tyr Pro Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg
            340   345   350

Glu Gly Leu Val Val Ile Asp Glu Thr Pro Ala Val Gly Val His Leu
            355   360   365

Asn Phe Met Ala Thr Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser
        370   375   380

Thr Trp Glu Lys Ile Arg Thr Phe Glu His His Gln Asp Val Leu Arg
385   390   395   400

Glu Leu Val Ser Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser
                405   410   415

Ile Ala Asn Glu Ala Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe
                420   425   430

Lys Pro Leu Val Glu Leu Thr Lys Glu Leu Asp Pro Gln Lys Arg Pro
            435   440   445

Val Thr Ile Val Leu Phe Val Met Ala Thr Pro Glu Thr Asp Lys Val
    450   455   460

Ala Glu Leu Ile Asp Val Ile Ala Leu Asn Arg Tyr Asn Gly Trp Tyr
465   470   475   480

Phe Asp Gly Gly Asp Leu Glu Ala Ala Lys Val His Leu Arg Gln Glu
            485   490   495

Phe His Ala Trp Asn Lys Arg Cys Pro Gly Lys Pro Ile Met Ile Thr
            500   505   510

Glu Tyr Gly Ala Asp Thr Val Ala Gly Phe His Asp Ile Asp Pro Val
            515   520   525

Met Phe Thr Glu Glu Tyr Gln Val Glu Tyr Tyr Gln Ala Asn His Val
    530   535   540

Val Phe Asp Glu Phe Glu Asn Phe Val Gly Glu Gln Ala Trp Asn Phe
545   550   555   560

Ala Asp Phe Ala Thr Ser Gln Gly Val Met Arg Val Gln Gly Asn Lys

```
                    565                      570                      575
    Lys Gly Val Phe Thr Arg Asp Arg Lys Pro Lys Leu Ala Ala His Val
            580                      585                      590

    Phe Arg Glu Arg Trp Thr Asn Ile Pro Asp Phe Gly Tyr Lys Asn
            595                      600                      605
```

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<210> 19
<211> 376
<212> PRT
<213> Staphylococcus hominis

<220>
<221> MOD_RES
<222> (209)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (351)
<223> Any amino acid

<400> 19
Gly Leu Ser Gly Asn Val Glu Ile Pro Asn Val Ile Leu Trp Glu Pro
  1               5                  10                  15

Leu Asn Thr Tyr Leu Tyr Gln Ile Lys Val Glu Leu Val Asn Asp Gly
                20                  25                  30

Leu Thr Ile Asp Val Tyr Glu Glu Pro Phe Gly Val Arg Thr Val Glu
            35                  40                  45

Val Asn Asp Gly Lys Phe Leu Ile Asn Asn Lys Pro Phe Tyr Phe Lys
        50                  55                  60

Gly Phe Gly Lys His Glu Asp Thr Pro Ile Asn Gly Arg Gly Phe Asn
 65                  70                  75                  80

Glu Ala Ser Asn Val Met Asp Phe Asn Ile Leu Lys Trp Ile Gly Ala
                85                  90                  95

Asn Ser Phe Arg Thr Ala His Tyr Pro Tyr Ser Glu Glu Leu Met Arg
                100                 105                 110

Leu Ala Asp Arg Glu Gly Leu Val Val Ile Asp Glu Thr Pro Ala Val
            115                 120                 125

Gly Val His Leu Asn Phe Met Ala Thr Thr Gly Leu Gly Glu Gly Ser
        130                 135                 140

Glu Arg Val Ser Thr Trp Glu Lys Ile Arg Thr Phe Glu His His Gln
145                 150                 155                 160

Asp Val Leu Arg Glu Leu Val Ser Arg Asp Lys Asn His Pro Ser Val
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Val Met Trp Ser Ile Ala Asn Glu Ala Ala Thr Glu Glu Glu Gly Ala
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Tyr Glu Tyr Phe Lys Pro Leu Gly Gly Ala Ala Lys Glu Leu Asp Pro
        195             200                 205

Xaa Lys Arg Pro Val Thr Ile Val Leu Phe Val Met Ala Thr Pro Glu
    210             215                 220

Thr Asp Lys Val Ala Glu Leu Ile Asp Val Ile Ala Leu Asn Arg Tyr
225             230                 235                 240

Asn Gly Trp Tyr Phe Asp Gly Gly Asp Leu Glu Ala Ala Lys Val His
            245                 250                 255

Leu Arg Gln Glu Phe His Ala Trp Asn Lys Arg Cys Pro Gly Lys Pro
        260             265                 270

Ile Met Ile Thr Glu Tyr Gly Ala Asp Thr Val Ala Gly Phe His Asp
        275             280                 285

Ile Asp Pro Val Met Phe Thr Glu Glu Tyr Gln Val Glu Tyr Tyr Gln
    290             295                 300

Ala Asn His Val Val Phe Asp Glu Phe Glu Asn Phe Val Gly Glu Gln
305             310                 315                 320

Ala Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Val Met Arg Val
            325             330                 335

Gln Gly Asn Lys Lys Gly Val Phe Thr Arg Asp Arg Lys Pro Xaa Leu
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Ala Ala His Val Phe Arg Glu Arg Arg Thr Asn Ile Pro Asp Phe Gly
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Tyr Lys Asn Ala Ser His His His
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             20                  25                  30

Asp Thr Trp Thr Xaa Ser Leu Leu Thr Glu Leu Ser Arg Leu Val Val
         35                  40                  45

Leu Ser Trp Thr Thr His Xaa Leu Thr Gly Glu Xaa Pro Ala Ile Ser
     50                  55                  60

Ile Leu Trp Pro Asn Ser Glu Leu Thr Val Ser Xaa Leu Tyr Xaa Gly
 65                  70                  75                  80

Ser Leu Xaa Ser Ser Ser Xaa Leu Cys Ser Ser Leu Thr Xaa His Val
             85                  90                  95

Val Ile Cys Gln Xaa Val Thr Leu Xaa Val Asp His Thr Gly Leu Ile
            100                 105                 110

Xaa Xaa Phe Glu Phe Met Ser Thr Thr Cys Cys Xaa Xaa Asp Glu Leu
        115                 120                 125

Val Thr Gly Thr Leu Ala Xaa Ile Leu Tyr His Xaa Ile Leu Pro His
        130                 135                 140
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Gly Leu Tyr Arg Lys Arg His Glu Xaa Gly Leu Gly Lys Xaa Asn Phe
145   150   155   160

Tyr Xaa Leu His Phe Ala Phe Phe Xaa Tyr Ala Xaa Leu Xaa Arg Thr
            165   170   175

Val Xaa Met Tyr Xaa Asn Leu Val Arg Xaa Gln Asp Ile Val Val Thr
        180   185   190

Xaa His Xaa Xaa Xaa Thr Val Glu Gln Cys Val Xaa Xaa Asn Lys Ile
    195   200   205

Xaa Ser Val Lys Ile Thr Ile Leu Asp Glu Asn Asp His Ala Ile Xaa
    210   215   220

Glu Ser Glu Gly Ala Lys Gly Asn Val Thr Ile Gln Asn Pro Ile Leu
225   230   235   240

Trp Gln Pro Leu His Ala Tyr Leu Tyr Asn Met Lys Val Glu Leu Leu
            245   250   255

Asn Asp Asn Glu Cys Val Asp Val Tyr Thr Glu Arg Phe Gly Ile Arg
        260   265   270

Ser Val Glu Val Lys Asp Gly Gln Phe Leu Ile Asn Asp Lys Pro Phe
    275   280   285

Tyr Phe Lys Gly Phe Gly Lys His Glu Asp Thr Tyr Asn Gly Arg Gly
    290   295   300

Leu Asn Glu Ser Ala Asn Val Met Asp Ile Asn Leu Met Lys Trp Ile
305   310   315   320

Gly Ala Asn Ser Phe Arg Thr Ser His Tyr Pro Tyr Ser Glu Glu Met
            325   330   335

Met Arg Leu Ala Asp Glu Gln Gly Ile Val Val Ile Asp Glu Thr Thr
        340   345   350

Xaa Val Gly Ile His Leu Asn Phe Met Xaa Thr Leu Gly Gly Ser Xaa
    355   360   365

Ala His Asp Thr Trp Xaa Glu Phe Asp Thr Leu Glu Phe His Lys Glu
    370   375   380

Val Ile Xaa Asp Leu Ile Xaa Arg Asp Lys Asn His Ala Trp Val Val
385   390   395   400

Met Trp Xaa Phe Gly Asn Glu Xaa Gly Xaa Asn Lys Gly Gly Ala Lys
        405   410   415

Ala Xaa Phe Glu Pro Phe Val Asn Leu Ala Gly Glu Lys Asp Xaa Xaa
        420   425   430

Xaa Xaa Pro Val Thr Ile Val Thr Ile Leu Xaa Ala Xaa Arg Asn Val
    435   440   445

Cys Glu Val Xaa Asp Leu Val Asp Val Val Cys Leu Xaa Xaa Xaa Xaa

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                 450                      455                      460

Gly Trp Tyr Xaa Gln Ser Gly Asp Leu Glu Gly Ala Lys Xaa Ala Leu
465                 470                 475                     480

Asp Lys Glu Xaa Xaa Glu Trp Trp Lys Xaa Gln Xaa Asn Lys Pro Xaa
                485                 490                     495

Met Phe Thr Glu Tyr Gly Val Asp Xaa Val Val Gly Leu Xaa Xaa Xaa
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Pro Asp Lys Met Xaa Pro Glu Glu Tyr Lys Met Xaa Phe Tyr Lys Gly
            515                 520                 525

Tyr Xaa Lys Ile Met Asp Lys
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                20                  25                  30

Pro Gly Ser Trp Asn Glu Gln Tyr Gln Asp Leu Cys Tyr Glu Glu Gly
            35                  40                  45

Pro Phe Thr Tyr Lys Thr Thr Phe Tyr Val Pro Lys Xaa Leu Ser Gln
    50                  55                  60

Lys His Ile Arg Leu Tyr Phe Ala Ala Val Asn Thr Asp Cys Glu Val
65                  70                  75                  80

Phe Leu Asn Gly Glu Lys Val Gly Glu Asn His Ile Glu Tyr Leu Pro
                85                  90                  95

Phe Glu Val Asp Val Thr Gly Lys Val Lys Ser Gly Glu Asn Glu Leu
                100                 105                 110

Arg Val Val Val Glu Asn Arg Leu Lys Val Gly Gly Phe Pro Ser Lys
            115                 120                 125

Val Pro Asp Ser Gly Thr His Thr Val Gly Phe Phe Gly Ser Phe Pro
    130                 135                 140

Pro Ala Asn Phe Asp Phe Phe Pro Tyr Gly Gly Ile Ile Arg Pro Val
145                 150                 155                 160
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Leu Ile Glu Phe Thr Asp His Ala Arg Ile Leu Asp Ile Trp Val Asp
                165   170   175

Thr Ser Glu Ser Glu Pro Glu Lys Lys Leu Gly Lys Val Lys Val Lys
            180   185   190

Ile Glu Val Ser Glu Glu Ala Val Gly Gln Glu Met Thr Ile Lys Leu
            195   200   205

Gly Glu Glu Glu Lys Lys Ile Arg Thr Ser Asn Arg Phe Val Glu Gly
    210   215   220

Glu Phe Ile Leu Glu Asn Ala Arg Phe Trp Ser Leu Glu Asp Pro Tyr
225   230   235   240

Leu Tyr Pro Leu Lys Val Glu Leu Glu Lys Asp Glu Tyr Thr Leu Asp
                245   250   255

Ile Gly Ile Arg Thr Ile Ser Trp Asp Glu Lys Arg Leu Tyr Leu Asn
                260   265   270

Gly Lys Pro Val Phe Leu Lys Gly Phe Gly Lys His Glu Glu Phe Pro
        275   280   285

Val Leu Gly Gln Gly Thr Phe Tyr Pro Leu Met Ile Lys Asp Phe Asn
    290   295   300

Leu Leu Lys Trp Ile Asn Ala Asn Ser Phe Arg Thr Ser His Tyr Pro
305   310   315   320

Tyr Ser Glu Glu Trp Leu Asp Leu Ala Asp Arg Leu Gly Ile Leu Val
            325   330   335

Ile Asp Glu Ala Pro His Val Gly Ile Thr Arg Tyr His Tyr Asn Pro
            340   345   350

Glu Thr Gln Lys Ile Ala Glu Asp Asn Ile Arg Arg Met Ile Asp Arg
        355   360   365

His Lys Asn His Pro Ser Val Ile Met Trp Ser Val Ala Asn Glu Pro
    370   375   380

Glu Ser Asn His Pro Asp Ala Glu Gly Phe Phe Lys Ala Leu Tyr Glu
385   390   395   400

Thr Ala Asn Glu Met Asp Arg Thr Arg Pro Val Val Met Val Ser Met
            405   410   415

Met Asp Ala Pro Asp Glu Arg Thr Arg Asp Val Ala Leu Lys Tyr Phe
        420   425   430

Asp Ile Val Cys Val Asn Arg Tyr Tyr Gly Trp Tyr Ile Tyr Gln Gly
        435   440   445

Arg Ile Glu Glu Gly Leu Gln Ala Leu Glu Lys Asp Ile Glu Glu Leu
    450   455   460

Tyr Ala Arg His Arg Lys Pro Ile Phe Val Thr Glu Phe Gly Ala Asp
465   470   475   480

Ala Ile Ala Gly Ile His Tyr Asp Pro Pro Gln Met Phe Ser Glu Glu
            485   490   495

Tyr Gln Ala Glu Leu Val Glu Lys Thr Ile Arg Leu Leu Leu Lys Lys
      500   505   510

Asp Tyr Ile Ile Gly Thr His Val Trp Ala Phe Ala Asp Phe Lys Thr
     515   520   525

Pro Gln Asn Val Arg Arg Pro Ile Leu Asn His Lys Gly Val Phe Thr
   530   535   540

Arg Asp Arg Gln Pro Lys Leu Val Ala His Val Leu Arg Arg Leu Trp
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Ser Glu Val

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        20   25   30

Val Gly Ala Asp Gly Asp Ile Arg Val Glu Leu Arg Asp Gly Gln Gln
     35   40   45

Gln Ile Val Ala Gln Gly Leu Gly Ala Thr Gly Ile Phe Glu Leu Asp
     50   55   60

Asn Pro His Leu Trp Glu Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Arg
65   70   75   80

Val Thr Cys Glu Ala Asn Gly Glu Cys Asp Glu Tyr Pro Val Arg Val
        85   90   95

Gly Ile Arg Ser Ile Thr Xaa Lys Gly Glu Gln Phe Leu Ile Asn His
        100   105   110

Lys Pro Phe Tyr Leu Thr Gly Phe Gly Arg His Glu Asp Ala Asp Phe
        115   120   125

Arg Gly Lys Gly Phe Asp Pro Val Leu Met Val His Asp His Ala Leu
  130   135   140

Met Asn Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr
145   150   155   160

Ala Glu Lys Met Leu Asp Trp Ala Asp Glu His Val Ile Val Val Ile
        165   170   175

Asn Glu Thr Ala Ala Gly Gly Phe Asn Thr Leu Ser Leu Gly Ile Thr
        180   185   190

Phe Asp Ala Gly Glu Arg Pro Lys Glu Leu Tyr Ser Glu Glu Ala Ile
        195   200   205

Asn Gly Glu Thr Ser Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu
  210   215   220

Ile Ala Arg Asp Lys Asn His Pro Ser Val Val Cys Trp Ser Ile Ala
225   230   235   240

Asn Glu Pro Asp Thr Arg Pro Asn Gly Ala Arg Glu Tyr Phe Ala Pro
        245   250   255

Leu Ala Lys Ala Thr Arg Glu Leu Asp Pro Thr Arg Pro Ile Thr Cys
        260   265   270

Val Asn Val Met Phe Cys Asp Ala Glu Ser Asp Thr Ile Thr Asp Leu
        275   280   285

Phe Asp Val Val Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser
  290   295   300

Gly Asp Leu Glu Lys Ala Glu Gln Met Leu Glu Gln Glu Leu Leu Ala
305   310   315   320

Trp Gln Ser Lys Leu His Arg Pro Ile Ile Ile Thr Glu Tyr Gly Val
        325   330   335

Asp Thr Leu Ala Gly Met Pro Ser Val Tyr Pro Asp Met Trp Ser Glu
        340   345   350

Lys Tyr Gln Trp Lys Trp Leu Glu Met Tyr His Arg Val Phe Asp Arg
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Gly Ser Val Cys
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Arg Trp Trp Glu Ser Ala Leu Gln Glu Ser Arg Ala Ile Ala Val Pro
        35                  40                  45

Gly Ser Phe Asn Asp Gln Phe Ala Asp Ala Asp Ile Arg Asn Tyr Ala
    50              55                  60

Gly Asn Val Trp Tyr Gln Arg Glu Val Phe Ile Pro Lys Gly Trp Ala
65              70                  75                  80

Gly Gln Arg Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr Gly Lys
            85                  90                  95

Val Trp Val Asn Asn Gln Glu Val Met Glu His Gln Gly Gly Tyr Thr
            100                 105                 110

Pro Phe Glu Ala Asp Val Thr Pro Tyr Val Ile Ala Gly Lys Ser Val
        115                 120                 125

Arg Ile Thr Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr Ile Pro
    130                 135             140

Pro Gly Met Val Ile Thr Asp Glu Asn Gly Lys Lys Lys Gln Ser Tyr
145                 150                 155                 160

Phe His Asp Phe Phe Asn Tyr Ala Gly Ile His Arg Ser Val Met Leu
                165                 170                 175

Tyr Thr Thr Pro Asn Thr Trp Val Asp Asp Ile Thr Val Val Thr His
            180                 185                 190

Val Ala Gln Asp Cys Asn His Ala Ser Val Asp Trp Gln Val Val Ala
            195                 200                 205

Asn Gly Asp Val Ser Val Glu Leu Arg Asp Ala Asp Gln Gln Val Val
    210                 215                 220

Ala Thr Gly Gln Gly Thr Ser Gly Thr Leu Gln Val Val Asn Pro His
225                 230                 235                 240

Leu Trp Gln Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Cys Val Thr Ala
            245                 250                 255

Lys Ser Gln Thr Glu Cys Asp Ile Tyr Pro Leu Arg Val Gly Ile Arg
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Ser Val Ala Val Lys Gly Glu Gln Phe Leu Ile Asn His Lys Pro Phe
            275                 280                 285
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Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly Lys
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Gly Phe Asp Asn Val Leu Met Val His Asp His Ala Leu Met Asp Trp
305             310             315                 320

Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu
                325             330                 335

Met Leu Asp Trp Ala Asp Glu His Gly Ile Val Val Ile Asp Glu Thr
            340             345             350

Ala Ala Val Gly Phe Asn Leu Ser Leu Gly Ile Gly Phe Glu Ala Gly
    355             360             365

Asn Lys Pro Lys Glu Leu Tyr Ser Glu Glu Ala Val Asn Gly Glu Thr
    370             375             380

Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp Lys
385             390             395             400

Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp Thr
            405             410             415

Arg Pro Gln Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Glu Ala Thr
    420             425             430

Arg Lys Leu Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met Phe
    435             440             445

Cys Asp Ala His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val Leu Cys
    450             455             460

Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu Thr
465             470             475             480

Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu
            485             490             495

His Gln Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala Gly
            500             505             510

Leu His Ser Met Tyr Thr Asp Met Trp Ser Glu Glu Tyr Gln Cys Ala
            515             520             525

Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val Val
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Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Ile
545             550             555             560

Leu Arg Val Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg Lys
                565             570             575

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gaaatcaaca actcgctgcg tgatggcatg aatcgcgtca ccgtcgccgt ggacaacatc 420
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gactttggcc ancttcctna accattcgca ncctccccca gtgggcttgt acacnattgn 480
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tccatctttg ctggcccaac agtgagttna cngtnncgna cnntnngang gatcagtgna 180
tcgagctccn ttnannttct ncgctaacat aacatgtngc atatgtcaat naatnacgct 240
ggncgtggan cncaccgggc tnattcgntg nnattcgaat tgnatgncaa caactntgnt 300
gcacgntggn aaanaattgc gtnacaggga ctttggccnc ttcctaaacc atngcatcct 360
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aggcngannt ttgacttttt caactatgca gnnctgcacc ggacgctgaa aatgtacang 480
accctgggta cgtncnacca agacatnnaa gtngtgaccg actccattgt nctaaccggg 540
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                             1               5

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Ile Asn Thr Glu Thr Arg Gly Val Phe Asp Leu Asn Gly Val Trp Asn
 10              15                  20                  25

ttc aag ctg gac tac ggg aaa gga ctg gaa gag aag tgg tac gaa agc   148
Phe Lys Leu Asp Tyr Gly Lys Gly Leu Glu Glu Lys Trp Tyr Glu Ser
             30              35                  40
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aag ctg acc gac act att agt atg gcc gtc cca agc agt tac aat gac    196
Lys Leu Thr Asp Thr Ile Ser Met Ala Val Pro Ser Ser Tyr Asn Asp
            45              50              55

att ggc gtg acc aag gaa atc cgc aac cat atc gga tat gtc tgg tac    244
Ile Gly Val Thr Lys Glu Ile Arg Asn His Ile Gly Tyr Val Trp Tyr
            60              65              70

gaa cgt gag ttc acg gtg ccg gcc tat ctg aag gat cag cgt atc gtg    292
Glu Arg Glu Phe Thr Val Pro Ala Tyr Leu Lys Asp Gln Arg Ile Val
    75              80              85

ctc cgc ttc ggc tct gca act cac aaa gca att gtc tat gtc aat ggt    340
Leu Arg Phe Gly Ser Ala Thr His Lys Ala Ile Val Tyr Val Asn Gly
 90              95             100             105

gag ctg gtc gtg gag cac aag ggc gga ttc ctg cca ttc gaa gcg gaa    388
Glu Leu Val Val Glu His Lys Gly Gly Phe Leu Pro Phe Glu Ala Glu
               110             115             120

atc aac aac tcg ctg cgt gat ggc atg aat cgc gtc acc gtc gcc gtg    436
Ile Asn Asn Ser Leu Arg Asp Gly Met Asn Arg Val Thr Val Ala Val
               125             130             135

gac aac atc ctc gac gat agc acc ctc ccg gtg ggg ctg tac agc gag    484
Asp Asn Ile Leu Asp Asp Ser Thr Leu Pro Val Gly Leu Tyr Ser Glu
           140             145             150

cgc cac gaa gag ggc ctc gga aaa gtc att cgt aac aag ccg aac ttc    532
Arg His Glu Glu Gly Leu Gly Lys Val Ile Arg Asn Lys Pro Asn Phe
   155             160             165

gac ttc ttc aac tat gca ggc ctg cac cgt ccg gtg aaa atc tac acg    580
Asp Phe Phe Asn Tyr Ala Gly Leu His Arg Pro Val Lys Ile Tyr Thr
170             175             180             185

acc ccg ttt acg tac gtc gag gac atc tcg gtt gtg acc gac ttc aat    628
Thr Pro Phe Thr Tyr Val Glu Asp Ile Ser Val Val Thr Asp Phe Asn
               190             195             200

ggc cca acc ggg act gtg acc tat acg gtg gac ttt caa ggc aaa gcc    676
Gly Pro Thr Gly Thr Val Thr Tyr Thr Val Asp Phe Gln Gly Lys Ala
           205             210             215

gag acc gtg aaa gtg tcg gtc gtg gat gag gaa ggc aaa gtg gtc gca    724
Glu Thr Val Lys Val Ser Val Val Asp Glu Glu Gly Lys Val Val Ala
           220             225             230

agc acc gag ggc ctg agc ggt aac gtg gag att ccg aat gtc atc ctc    772
Ser Thr Glu Gly Leu Ser Gly Asn Val Glu Ile Pro Asn Val Ile Leu
   235             240             245

tgg gaa cca ctg aac acg tat ctc tac cag atc aaa gtg gaa ctg gtg    820
Trp Glu Pro Leu Asn Thr Tyr Leu Tyr Gln Ile Lys Val Glu Leu Val
250             255             260             265

aac gac gga ctg acc atc gat gtc tat gaa gag ccg ttc ggc gtg cgg    868
Asn Asp Gly Leu Thr Ile Asp Val Tyr Glu Glu Pro Phe Gly Val Arg
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270   275   280

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acc gtg gaa gtc aac gac ggc aag ttc ctc atc aac aac aaa ccg ttc    916
Thr Val Glu Val Asn Asp Gly Lys Phe Leu Ile Asn Asn Lys Pro Phe
        285                290                295

tac ttc aag ggc ttt ggc aaa cat gag gac act cct atc aac ggc cgt    964
Tyr Phe Lys Gly Phe Gly Lys His Glu Asp Thr Pro Ile Asn Gly Arg
        300                305                310

ggc ttt aac gaa gcg agc aat gtg atg gat ttc aat atc ctc aaa tgg    1012
Gly Phe Asn Glu Ala Ser Asn Val Met Asp Phe Asn Ile Leu Lys Trp
        315                320                325

atc ggc gcc aac agc ttc cgg acc gca cac tat ccg tac tct gaa gag    1060
Ile Gly Ala Asn Ser Phe Arg Thr Ala His Tyr Pro Tyr Ser Glu Glu
330                335                340                345

ttg atg cgt ctt gcg gat cgc gag ggt ctg gtc gtg atc gac gag act    1108
Leu Met Arg Leu Ala Asp Arg Glu Gly Leu Val Val Ile Asp Glu Thr
                350                355                360

ccg gca gtt ggc gtg cac ctc aac ttc atg gcc acc acg gga ctc ggc    1156
Pro Ala Val Gly Val His Leu Asn Phe Met Ala Thr Thr Gly Leu Gly
            365                370                375

gaa ggc agc gag cgc gtc agt acc tgg gag aag att cgg acg ttt gag    1204
Glu Gly Ser Glu Arg Val Ser Thr Trp Glu Lys Ile Arg Thr Phe Glu
        380                385                390

cac cat caa gac gtt ctc cgt gaa ctg gtg tct cgt gac aag aac cat    1252
His His Gln Asp Val Leu Arg Glu Leu Val Ser Arg Asp Lys Asn His
    395                400                405

cca agc gtc gtg atg tgg agc atc gcc aac gag gcg gcg act gag gaa    1300
Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Ala Ala Thr Glu Glu
410                415                420                425

gag ggc gcg tac gag tac ttc aag ccg ttg gtg gag ctg acc aag gaa    1348
Glu Gly Ala Tyr Glu Tyr Phe Lys Pro Leu Val Glu Leu Thr Lys Glu
            430                435                440

ctc gac cca cag aag cgt ccg gtc acg atc gtg ctg ttt gtg atg gct    1396
Leu Asp Pro Gln Lys Arg Pro Val Thr Ile Val Leu Phe Val Met Ala
        445                450                455

acc ccg gag acg gac aaa gtc gcc gaa ctg att gac gtc atc gcg ctc    1444
Thr Pro Glu Thr Asp Lys Val Ala Glu Leu Ile Asp Val Ile Ala Leu
        460                465                470

aat cgc tat aac gga tgg tac ttc gat ggc ggt gat ctc gaa gcg gcc    1492
Asn Arg Tyr Asn Gly Trp Tyr Phe Asp Gly Gly Asp Leu Glu Ala Ala
    475                480                485

aaa gtc cat ctc cgc cag gaa ttt cac gcg tgg aac aag cgt tgc cca    1540
Lys Val His Leu Arg Gln Glu Phe His Ala Trp Asn Lys Arg Cys Pro
490                495                500                505
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Gly Lys Pro Ile Met Ile Thr Glu Tyr Gly Ala Asp Thr Val Ala Gly
            510             515             520

ttt cac gac att gat cca gtg atg ttc acc gag gaa tat caa gtc gag    1636
Phe His Asp Ile Asp Pro Val Met Phe Thr Glu Glu Tyr Gln Val Glu
            525             530             535

tac tac cag gcg aac cac gtc gtg ttc gat gag ttt gag aac ttc gtg    1684
Tyr Tyr Gln Ala Asn His Val Val Phe Asp Glu Phe Glu Asn Phe Val
            540             545             550

ggt gag caa gcg tgg aac ttc gcg gac ttc gcg acc tct cag ggc gtg    1732
Gly Glu Gln Ala Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Val
            555             560             565

atg cgc gtc caa gga aac aag aag ggc gtg ttc act cgt gac cgc aag    1780
Met Arg Val Gln Gly Asn Lys Lys Gly Val Phe Thr Arg Asp Arg Lys
570             575             580             585

ccg aag ctc gcc gcg cac gtc ttt cgc gag cgc tgg acc aac att cca    1828
Pro Lys Leu Ala Ala His Val Phe Arg Glu Arg Trp Thr Asn Ile Pro
            590             595             600

gat ttc ggc tac aag aac gct agc cat cac cat cac cat cac gtg tga    1876
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attggtgacc g                                                       1887
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Gly Leu Glu Glu Lys Trp Tyr Glu Ser Lys Leu Thr Asp Thr Ile Ser
            35              40              45

Met Ala Val Pro Ser Ser Tyr Asn Asp Ile Gly Val Thr Lys Glu Ile
    50              55              60

Arg Asn His Ile Gly Tyr Val Trp Tyr Glu Arg Glu Phe Thr Val Pro
65              70              75              80

Ala Tyr Leu Lys Asp Gln Arg Ile Val Leu Arg Phe Gly Ser Ala Thr
            85              90              95

His Lys Ala Ile Val Tyr Val Asn Gly Glu Leu Val Val Glu His Lys
            100             105             110
```

```
Gly Gly Phe Leu Pro Phe Glu Ala Glu Ile Asn Asn Ser Leu Arg Asp
        115             120                 125

Gly Met Asn Arg Val Thr Val Ala Val Asp Asn Ile Leu Asp Asp Ser
        130             135                 140

Thr Leu Pro Val Gly Leu Tyr Ser Glu Arg His Glu Glu Gly Leu Gly
145             150                 155                     160

Lys Val Ile Arg Asn Lys Pro Asn Phe Asp Phe Phe Asn Tyr Ala Gly
                165             170                 175

Leu His Arg Pro Val Lys Ile Tyr Thr Thr Pro Phe Thr Tyr Val Glu
            180             185                 190

Asp Ile Ser Val Val Thr Asp Phe Asn Gly Pro Thr Gly Thr Val Thr
        195             200                 205

Tyr Thr Val Asp Phe Gln Gly Lys Ala Glu Thr Val Lys Val Ser Val
    210             215                 220

Val Asp Glu Glu Gly Lys Val Val Ala Ser Thr Glu Gly Leu Ser Gly
225             230                 235                     240

Asn Val Glu Ile Pro Asn Val Ile Leu Trp Glu Pro Leu Asn Thr Tyr
                245             250                 255

Leu Tyr Gln Ile Lys Val Glu Leu Val Asn Asp Gly Leu Thr Ile Asp
            260             265                 270

Val Tyr Glu Glu Pro Phe Gly Val Arg Thr Val Glu Val Asn Asp Gly
    275                 280                 285

Lys Phe Leu Ile Asn Asn Lys Pro Phe Tyr Phe Lys Gly Phe Gly Lys
    290                 295                 300

His Glu Asp Thr Pro Ile Asn Gly Arg Gly Phe Asn Glu Ala Ser Asn
305                 310                 315                 320

Val Met Asp Phe Asn Ile Leu Lys Trp Ile Gly Ala Asn Ser Phe Arg
                325             330                 335

Thr Ala His Tyr Pro Tyr Ser Glu Glu Leu Met Arg Leu Ala Asp Arg
            340             345                 350

Glu Gly Leu Val Val Ile Asp Glu Thr Pro Ala Val Gly Val His Leu
        355             360                 365

Asn Phe Met Ala Thr Thr Gly Leu Gly Glu Gly Ser Glu Arg Val Ser
    370             375                 380

Thr Trp Glu Lys Ile Arg Thr Phe Glu His His Gln Asp Val Leu Arg
385                 390                 395                 400

Glu Leu Val Ser Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser
            405                 410                 415

Ile Ala Asn Glu Ala Ala Thr Glu Glu Glu Gly Ala Tyr Glu Tyr Phe
```

```
                    420                      425                      430

    Lys Pro Leu Val Glu Leu Thr Lys Glu Leu Asp Pro Gln Lys Arg Pro
            435                      440                      445

    Val Thr Ile Val Leu Phe Val Met Ala Thr Pro Glu Thr Asp Lys Val
            450                      455                      460

    Ala Glu Leu Ile Asp Val Ile Ala Leu Asn Arg Tyr Asn Gly Trp Tyr
    465                      470                      475                      480

    Phe Asp Gly Gly Asp Leu Glu Ala Ala Lys Val His Leu Arg Gln Glu
                    485                      490                      495

    Phe His Ala Trp Asn Lys Arg Cys Pro Gly Lys Pro Ile Met Ile Thr
                    500                      505                      510

    Glu Tyr Gly Ala Asp Thr Val Ala Gly Phe His Asp Ile Asp Pro Val
            515                      520                      525

    Met Phe Thr Glu Glu Tyr Gln Val Glu Tyr Tyr Gln Ala Asn His Val
            530                      535                      540

    Val Phe Asp Glu Phe Glu Asn Phe Val Gly Glu Gln Ala Trp Asn Phe
    545                      550                      555                      560

    Ala Asp Phe Ala Thr Ser Gln Gly Val Met Arg Val Gln Gly Asn Lys
                    565                      570                      575

    Lys Gly Val Phe Thr Arg Asp Arg Lys Pro Lys Leu Ala Ala His Val
                    580                      585                      590

    Phe Arg Glu Arg Trp Thr Asn Ile Pro Asp Phe Gly Tyr Lys Asn Ala
            595                      600                      605

    Ser His His His His His Val
    .   610                      615
```

```
<210> 29
<211> 16
<212> PRT
<213> Bacillus sp.

<400> 29
Met Leu Ile Ile Thr Cys Asn His Leu His Leu Lys Arg Ser Ala Ile
1               5                      10                      15


<210> 30
<211> 4
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Illustrative
      peptide
```

```
<400> 30
Lys Asp Glu Leu
   1


<210> 31
<211> 6
<212> PRT
<213> Escherichia coli

<400> 31
Asp Phe Phe Asn Tyr Ala
   1               5


<210> 32
<211> 5
<212> PRT
<213> Escherichia coli

<400> 32
Trp Asn Phe Ala Asp
   1               5


<210> 33
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
ayttyttyaa ytaygc                                                16


<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (7)
<223> inosine

<400> 34
gaartcngcr aarttcca                                              18


<210> 35
<211> 17
<212> DNA
<213> Artificial Sequence
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```
<220>
<223> Description of Artificial Sequence: Primer

<400> 35
atcgcacgtc ccactac                                              17


<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
cgtgcgatag gagttagc                                            18


<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
atttagaaca tctcattatc cc                                       22


<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
tgagatgttc taaatgaatt agc                                      23


<210> 39
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
atcgtgaccg gacgctt                                             17


<210> 40
<211> 17
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```
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 40
gcgcgtaatc ttcctgg                                              17


<210> 41
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 41
tagcgacctt cgctttcgg                                            19


<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
atcatgttta cagagtatgg                                           20


<210> 43
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 43
ggaatattgc acaatgggcg c                                         21


<210> 44
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 44
gatctctacg catttcaccg cta                                       23
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<210> 45
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
atggtaagac cgcaacg                                                    17


<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 46
taaaaaccat ggtaagaccg caacg                                           25


<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
cctcactcca cagtcttctc                                                 20


<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
agaccgctag cctcactcca cagtcttctc                                      30


<210> 49
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
tttgactttt tcaactatgc ag                                              22
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```
<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
aattctgcat agttgaaaaa gtc                                              23


<210> 51
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 51
gtcgacccat ggtagatctg actagtctgt acccg                                 35


<210> 52
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 52
gtcgacagga gtgctatcat gctgtacccg                                       30


<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 53
gtcgacagga gtgctaccat ggtgtacccg                                       30


<210> 54
<211> 36
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 54
gtcgacagga gtgctaccat ggtagatctg tacccg                              36


<210> 55
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 55
gctagccatc accatcacca tcacgtgtga attggtgacc g                        41


<210> 56
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 56
Ser Ser His His His His His His Val
  1               5


<210> 57
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 57
tcgacccatg gtagatctga ctagtctgta cccgatcaac accgagaccc gtggcgtctt   60
cgacctcaat ggcgtctgga                                                80


<210> 58
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide
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95

95

<400> 58
ggatttcctt ggtcacgcca atgtcattgt aactgcttgg gacggccata ctaatagtgt 60
cggtcagctt gctttcgtac 80

<210> 59
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 59
ccaagcagtt acaatgacat tggcgtgacc aaggaaatcc gcaaccatat cggatatgtc 60
tggtacgaac gtgagttcac 80

<210> 60
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 60
gcggagcacg atacgctgat ccttcagata ggccggcacc gtgaactcac gttcgtacca 60
gacatatccg atatggttgc 80

<210> 61
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 61
ggtgccggcc tatctgaagg atcagcgtat cgtgctccgc ttcggctctg caactcacaa 60
agcaattgtc tatgtcaatg 80

<210> 62
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 62
aatggcagga atccgccctt gtgctccacg accagctcac cattgacata gacaattgct 60

ttgtgagttg cagagccgaa   80

<210> 63
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 63
gtgagctggt cgtggagcac aagggcggat tcctgccatt cgaagcggaa atcaacaact 60
cgctgcgtga tggcatgaat   80

<210> 64
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 64
gtacagcccc accggtaggg tgctatcgtc gaggatgttg tccacggcga cggtgacgcg 60
attcatgcca tcacgcagcg agttgttgat ttccgcttcg   100

<210> 65
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 65
cgcgtcaccg tcgccgtgga caacatcctc gacgatagca ccctaccggt ggggct   56

<210> 66
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 66
cacttctctt ccagtccttt cccgtagtcc agcttgaagt tccagacgcc attgaggtcg 60
aagacgccac gggtctcggt   80

<210> 67
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 67
ttgatcgggt acagactagt cagatctacc atggg   35

<210> 68
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 68
acttcaagct ggactacggg aaaggactgg aagagaagtg gtacgaaagc aagctgaccg 60
acactattag tatggccgtc   80

<210> 69
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 69
gtacagcgag cgccacgaag agggcctcgg aaaagtcatt cgtaacaagc cgaacttcga 60
cttcttcaac tatgcaggcc   80

<210> 70
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 70
ctttgccttg aaagtccacc gtataggtca cagtcccggt tgggccattg aagtcggtca 60
caaccgagat gtcctcgacg   80

<210> 71
<211> 80
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 71
accgggactg tgacctatac ggtggacttt caaggcaaag ccgagaccgt gaaagtgtcg 60
gtcgtggatg aggaaggcaa   80

<210> 72
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 72
ctccacgtta ccgctcaggc cctcggtgct tgcgaccact ttgccttcct catccacgac 60
cgacactttc acggtctcgg   80

<210> 73
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 73
agtggtcgca agcaccgagg gcctgagcgg taacgtggag attccgaatg tcatcctctg 60
ggaaccactg aacacgtatc   80

<210> 74
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 74
gtcagtccgt cgttcaccag ttccactttg atctggtaga gatacgtgtt cagtggttcc 60
cagaggatga cattcggaat   80

<210> 75
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 75
tctaccagat caaagtggaa ctggtgaacg acggactgac catcgatgtc tatgaagagc 60
cgttcggcgt gcggaccgtg   80

<210> 76
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 76
acggtttgtt gttgatgagg aacttgccgt cgttgacttc cacggtccgc acgccgaacg 60
gctcttcata gacatcgatg   80

<210> 77
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 77
gaagtcaacg acggcaagtt cctcatcaac aacaaaccgt tctacttcaa gggctttggc 60
aaacatgagg acactcctat   80

<210> 78
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 78
tacgtaaacg gggtcgtgta gattttcacc ggacggtgca ggcctgcata gttgaagaag 60
tcgaagttcg gcttgttacg   80

<210> 79
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 79
atccatcaca ttgctcgctt cgttaaagcc acggccgttg ataggagtgt cctcatgttt 60
gccaaagccc ttgaagtaga. 80

<210> 80
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide·

<400> 80
caacggccgt ggctttaacg aagcgagcaa tgtgatggat ttcaatatcc tcaaatggat 60
cggcgccaac agctt 75

<210> 81
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide

<400> 81
aatgactttt ccgaggccct cttcgtggcg ctcgct 36

<210> 82
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide

<400> 82
ccggaagctg ttggcgccga tccatttgag gatattgaa 39

<210> 83
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide

<400> 83
tgcaccgtcc ggtgaaaatc tacacgaccc cgtttacgta cgtcgaggac atctcggttg 60

tgaccgactt caatggccca   80

<210> 84
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 84
ccggaccgca cactatccgt actctgaaga gttgatgcgt cttgcggatc gcgagggtct 60
ggtcgtgatc gacgagactc   80

<210> 85
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 85
gttcacggag aacgtcttga tggtgctcaa acgtccgaat cttctcccag gtactgacgc 60
gctcgctgcc ttcgccgagt   80

<210> 86
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 86
attcggacgt ttgagcacca tcaagacgtt ctccgtgaac tggtgtctcg tgacaagaac 60
catccaagcg tcgtgatgtg   80

<210> 87
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 87
cgcgccctct tcctcagtcg ccgcctcgtt ggcgatgctc cacatcacga cgcttggatg 60
gttcttgtca cgagacacca   80

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<210> 88
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 88
gagcatcgcc aacgaggcgg cgactgagga agagggcgcg tacgagtact tcaagccgtt 60
ggtggagctg accaaggaac                                            80


<210> 89
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 89
acaaacagca cgatcgtgac cggacgcttc tgtgggtcga gttccttggt cagctccacc 60
aacggcttga agtactcgta                                            80


<210> 90
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 90
tcgacccaca gaagcgtccg gtcacgatcg tgctgtttgt gatggctacc ccggagacgg 60
acaaagtcgc cgaactgatt                                            80


<210> 91
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 91
cgaagtacca tccgttatag cgattgagcg cgatgacgtc aatcagttcg gcgactttgt 60
ccgtctccgg ggtagccatc                                            80


<210> 92
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```
<211> 89
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 92
gacgtcatcg cgctcaatcg ctataacgga tggtacttcg atggcggtga tctcgaagcg 60
gccaaagtcc atctccgcca ggaatttca                                     89


<210> 93
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 93
cccgtggtgg ccatgaagtt gaggtgcacg ccaactgccg gagtctcgtc gatcacgacc 60
agaccctcgc gatccgcaag                                               80


<210> 94
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 94
cgcgtgaaat tcctggcgga gatggacttt ggccgcttcg agatcaccgc cat          53


<210> 95
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 95
acgcatcaac tcttcagagt acggatagtg tgcggt                             36


<210> 96
<211> 80
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 96
cggcagttgg cgtgcacctc aacttcatgg ccaccacggg actcggcgaa ggcagcgagc 60
gcgtcagtac ctgggagaag                                            80


<210> 97
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 97
cgcgtggaac aagcgttgcc caggaaagcc gatcatgatc actgagtacg gcgcagacac 60
cgttgcgggc tttcacgaca                                            80


<210> 98
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 98
tcgcgaagtc cgcgaagttc cacgcttgct cacccacgaa gttctcaaac tcatcgaaca 60
cgacgtggtt cgcctggtag                                            80


<210> 99
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 99
ttcgtgggtg agcaagcgtg gaacttcgcg gacttcgcga cctctcaggg cgtgatgcgc 60
gtccaaggaa acaagaaggg                                            80


<210> 100
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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oligonucleotide

<400> 100
gtgcgcggcg agcttcggct tgcggtcacg agtgaacacg cccttcttgt ttccttggac 60
gcgcatcacg ccctgagagg 80

<210> 101
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 101
cgtgttcact cgtgaccgca agccgaagct cgccgcgcac gtctttcgcg agcgctggac 60
caacattcca gatttcggct 80

<210> 102
<211> 89
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 102
cggtcaccaa ttcacacgtg atggtgatgg tgatggctag cgttcttgta gccgaaatct 60
ggaatgttgg tccagcgctc gcgaaagac 89

<210> 103
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 103
acaagaacgc tagccatcac catcaccatc acgtgtgaat tggtgaccgg gcc 53

<210> 104
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 104

tactcgactt gatattcctc ggtgaacatc actggatcaa tgtcgtgaaa gcccgcaacg 60
gtgtctgcgc cgtactcagt   80

<210> 105
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 105
gatcatgatc ggctttcctg ggcaacgctt gttcca   36

<210> 106
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 106
ttgatccagt gatgttcacc gaggaatatc aagtcgagta ctaccaggcg aaccacgtcg 60
tgttcgatga gtttgagaac   80

<210> 107
<211> 60
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Invertase signal
      sequence used in yeast vector

<400> 107
atgcttttgc aagccttcct tttccttttg gctggttttg cagccaaaat atctgcaatg 60

<210> 108
<211> 258
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Mat alpha signal
      sequence used in yeast vector

<400> 108
atgagatttc cttcaatttt tactgcagtt ttattcgcag catcctccgc attagctgct 60
ccagtcaaca ctacaacaga agatgaaacg gcacaaattc cggctgaagc tgtcatcggt 120
tacttagatt tagaagggga tttcgatgtt gctgttttgc cattttccaa cagcacaaat 180
aacgggttat tgtttataaa tactactatt gccagcattg ctgctaaaga agaagggggta 240

tctttggata aaagagag   258

<210> 109
<211> 88
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Extensin signal
     sequence used in plant vector

<400> 109
catgggaaaa atggcttctc tatttgccac atttttagtg gttttagtgt cacttagctt 60
agcttctgaa agctcagcaa attatcaa   88

<210> 110
<211> 82
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: GRP signal
     sequence used in plant vector

<400> 110
catggctact actaagcatt tggctcttgc catccttgtc ctccttagca ttggtatgac 60
caccagtgca agaaccctcc ta   82

<210> 111
<211> 43
<212> DNA
<213> Artificial Sequence

.<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide

<220>
<221> modified_base
<222> (26)..(27)
<223> a, c, t, g, other or unknown

<400> 111
attcctgcca ttcgaggcgg aaatcnngaa ctcgctgcgt gat   43

<210> 112
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     oligonucleotide

<220>
<221> modified_base
<222> (17)..(18)
<223> a, c, t, g, other or unknown

<400> 112
atcacgcagc gagttcnnga tttccgcctc gaatggcagg aat   43

<210> 113
<211> 1812
<212> DNA
<213> Salmonella sp.

<400> 113
atgttacgtt ctgtcgaaac cgcgacgcga gaaatcaaaa aactggacgg cctgtggtcg 60
ttttgtatgg atagcgaaga gtgcggcaac gcgcagcaat ggtggcgtca accgttaccc 120
caaagccgcg ctatcgccgt tccgggaagc tataacgatc agtttgccgc tgccgagatc 180
cgcaattatg ttggcaacgt ctggtatcag cgtgagatac gcatcccgaa aggctgggat 240
cgccagcgca tagtgctgcg ctttgatgcg gtgactcact atggaaaagt ttgggtcaat 300
gaccaatttt taatggaaca tcagggcggc tacacgccgt ttgaagcgga tatcagccac 360
cttatctccg ccggggaatc cgtgcgtatc acggtatgcg tgaataacga gctgaactgg 420
cagacgatcc cgccgggcgt tgtgacccag ggcgtaaacg gtaagaagca gcaagcgtat 480
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aaaacttttg tggaagatat taccgtcgtg acgcaggttg ctgacgatct ggctcaggct 600
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caacagcttg tcgcttcggg gcaaggggaa aaaggtgaac tgctgctgga agggccgcgg 720
ctgtggcagc ctggcgaggg ctatctttat gaactgcggg tcatcgcgca gcatcaggac 780
gagcaggatg aatatccgct cgcgtcggt attcgctcgg tagaagtaaa aggggagcag 840
ttcctgatca accataagcc tttctatttc accgggttcg gacgtcatga agatgccgat 900
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atcggtgcga actcttaccg tacctcgcat tacccttatg ccgaagagat gctcgactgg 1020
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ttagggatta gctttgatgt cggcgaaaaa cccaaagagc tctacagcga tgaggccgtg 1140
aacgatgaaa cgcagcgcgc gcacctgcag gcaattaagg agctgattgc ccgcgataag 1200
aaccacccaa gcgtcgtgat gtggagtatc gccaacgaac cggatacccg cccgaacggc 1260
gcgcgcgaat acttcgctcc gctggcgcag gcaacgcgcg aactcgatcc tacacgtccg 1320
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gatgtcgttt gcctgaaccg ctactacggc tggtatgtac aaagcggcga tctggagaag 1440
gctgagaaag tgctggagaa agagcttctg gcctggcagg agaaactcca ccgcccgatt 1500
atcatcaccg aatacggcgt cgatacgctt gcaggcctgc attccatgta caacgatatg 1560
tggagcgaag agtaccagtg cgcctggctt gatatgtacc atcgcgtgtt tgatcgcgtc 1620
agcgccgtcg tcggcgagca ggtatggaac ttcgccgact cgccacttc gcagggcatt 1680
atgcgcgttg cggcaacaa aaaaggtata ttcacccgcg acagaaaacc aaaatcggcg 1740
gccttcctgc tgcaaaaacg ctggaccggc atggactttg cgtgaagcc ccagcaggga 1800
gataaataat ga   1812

<210> 114
<211> 602
<212> PRT
<213> Salmonella sp.

<400> 114
Met Leu Arg Ser Val Glu Thr Ala Thr Arg Glu Ile Lys Lys Leu Asp
1   5   10   15

Gly Leu Trp Ser Phe Cys Met Asp Ser Glu Glu Cys Gly Asn Ala Gln

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                    20                          25                          30

Gln Trp Trp Arg Gln Pro Leu Pro Gln Ser Arg Ala Ile Ala Val Pro
            35                  40                  45

Gly Ser Tyr Asn Asp Gln Phe Ala Ala Ala Glu Ile Arg Asn Tyr Val
        50                  55                  60

Gly Asn Val Trp Tyr Gln Arg Glu Ile Arg Ile Pro Lys Gly Trp Asp
65                  70                  75                  80

Arg Gln Arg Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr Gly Lys
                85                  90                  95

Val Trp Val Asn Asp Gln Phe Leu Met Glu His Gln Gly Gly Tyr Thr
            100                 105                 110

Pro Phe Glu Ala Asp Ile Ser His Leu Ile Ser Ala Gly Glu Ser Val
        115                 120                 125

Arg Ile Thr Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr Ile Pro
    130                 135                 140

Pro Gly Val Val Thr Gln Gly Val Asn Gly Lys Lys Gln Gln Ala Tyr
145                 150                 155                 160

Phe His Asp Phe Phe Asn Tyr Ala Gly Ile His Arg Ser Val Met Leu
            165                 170                 175

Tyr Thr Thr Pro Lys Thr Phe Val Glu Asp Ile Thr Val Val Thr Gln
        180                 185                 190

Val Ala Asp Asp Leu Ala Gln Ala Thr Val Ala Trp Gln Val Arg Ala
        195                 200                 205

Asn Gly Glu Val Arg Val Glu Leu Arg Asp Ala Glu Gln Gln Leu Val
    210                 215                 220

Ala Ser Gly Gln Gly Glu Lys Gly Glu Leu Leu Leu Glu Gly Pro Arg
225                 230                 235                 240

Leu Trp Gln Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Arg Val Ile Ala
            245                 250                 255

Gln His Gln Asp Glu Gln Asp Glu Tyr Pro Leu Arg Val Gly Ile Arg
            260                 265                 270

Ser Val Glu Val Lys Gly Glu Gln Phe Leu Ile Asn His Lys Pro Phe
        275                 280                 285

Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg Gly Lys
    290                 295                 300

Gly Phe Asp Asn Val Leu Met Val His Asp His Ala Leu Met Asp Trp
305                 310                 315                 320

Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu
            325                 330                 335
```

Met Leu Asp Trp Ala Asp Glu His Gly Ile Val Ile Ile Asp Glu Thr
        340   345   350

Ala Ala Val Gly Phe Asn Leu Ser Leu Gly Ile Ser Phe Asp Val Gly
        355   360   365

Glu Lys Pro Lys Glu Leu Tyr Ser Asp Glu Ala Val Asn Asp Glu Thr
    370   375   380

Gln Arg Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg Asp Lys
385   390   395   400

Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro Asp Thr
            405   410   415

Arg Pro Asn Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Gln Ala Thr
            420   425   430

Arg Glu Leu Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val Met Phe
        435   440   445

Cys Asp Ala Glu Ser Asp Thr Ile Thr Asp Leu Phe Asp Val Val Cys
    450   455   460

Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu Glu Lys
465   470   475   480

Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala Trp Gln Glu Lys Leu
            485   490   495

His Arg Pro Ile Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu Ala Gly
        500   505   510

Leu His Ser Met Tyr Asn Asp Met Trp Ser Glu Glu Tyr Gln Cys Ala
    515   520   525

Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg Val Ser Ala Val Val
    530   535   540

Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln Gly Ile
545   550   555   560

Met Arg Val Gly Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp Arg Lys
            565   570   575

Pro Lys Ser Ala Ala Phe Leu Leu Gln Lys Arg Trp Thr Gly Met Asp
        580   585   590

Phe Gly Val Lys Pro Gln Gln Gly Asp Lys
        595   600

<210> 115
<211> 1822
<212> DNA
<213> Staphylococcus sp.

<400> 115
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agcaagctga ccgacactat tagtatggcc gtcccaagca gttacaatga cattggcgtg 180
accaaggaaa tccgcaacca tatcggatat gtctggtacg aacgtgagtt cacggtgccg 240
gcctatctga aggatcagcg tatcgtgctc cgcttcggct ctgcaactca caaagcaatt 300
gtctatgtca atggtgagct ggtcgtggag cacaagggcg gattcctgcc attcgaagcg 360
gaaatcaaca actcgctgcg tgatggcatg aatcgcgtca ccgtcgccgt ggacaacatc 420
ctcgacgata gcacccuccc ggtggggctg tacagcgagc gccacgaaga gggcctcgga 480
aaagtcattc gtaacaagcc gaacttcgac ttcttcaact atgcaggcct gcaccgtccg 540
gtgaaaatct acgacccc gtttacgtac gtcgaggaca tctcggttgt gaccgacttc 600
aatggcccaa ccgggactgt gacctatacg gtggactttc aaggcaaagc cgagaccgtg 660
aaagtgtcgg tcgtggatga ggaaggcaaa gtggtcgcaa gcaccgaggg cctgagcggt 720
aacgtggaga ttccgaatgt catcctctgg gaaccactga acacgtatct ctacccagat 780
caaagtggaa ctggtgaacg acggactgac catcgatgtc tatgaagagc cgttcggcgt 840
gcggaccgtg gaagtcaacg acggcaagtt cctcatcaac aacaaaccgt tctacttcaa 900
gggctttggc aaacatgagg acactcctat caacggccgt ggctttaacg aagcgagcaa 960
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tgaactggtg tctcgtgaca agaaccatcc aagcgtcgtg atgtggagca tcgccaacga 1260
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ggaactcgac ccacagaagc gtccggtcac gatcgtgctg tttgtgatgg ctaccccgga 1380
gacggacaaa gtcgccgaac tgattgacgt catcgcgctc aatcgctata acggatggta 1440
cttcgatggc ggtgatctcg aagcggccaa agtccatctc cgccaggaat tcacgcgtg 1500
gaacaagcgt tgcccaggaa agccgatcat gatcactgag tacggcgcag acaccgttgc 1560
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cgcggacttc gcgacctctc agggcgtgat gcgcgtccaa ggaaacaaga agggcgtgtt 1740
cactcgtgac cgcaagccga agctcgccgc gcacgtcttt cgcgagcgct ggaccaacat 1800
tccagatttc ggctacaaga ac                                        1822
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<210> 116
<211> 1980
<212> DNA
<213> Escherichia coli

<400> 116
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caaaaaactc gacggcctgt gggcattcag tctggatcgc gaaaactgtg gaattgatca 120
gcgttggtgg gaaagcgcgt tacaagaaag ccgggcaatt gctgtgccag gcagtttaa 180
cgatcagttc gccgatgcag atattcgtaa ttatgcgggc aacgtctggt atcagcgcga 240
agtctttata ccgaaaggtt gggcaggcca gcgtatcgtg ctgcgtttcg atgcggtcac 300
tcattacggc aaagtgtggg tcaataatca ggaagtgatg gaccatcagg cggctatac 360
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ttctgtgaac aacgaactga actggcagac tatcccgccg ggaatggtga ttaccgacga 480
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cagcgtaatg ctctacacca cgccgaacac ctgggtggac gatatcaccg tggtgacgca 600
tgtcgcgcaa gactgtaacc acgcgtctgt tgactggcag gtggtggcca atggtgatgt 660
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taaagagctg atagcgcgtg acaaaaacca cccaagcgtg gtgatgtgga gtattgccaa 1260
cgaaccggat acccgtccgc aagtgcacgg gaatatttcg ccactggcgg aagcaacgcg 1320
taaactcgac ccgacgcgtc cgatcacctg cgtcaatgta atgttctgcg acgctcacac 1380
cgataccatc agcgatctct ttgatgtgct gtggctgaac cgttattacg gatggtatgt 1440
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gtcggctaca gcctcggtga cgtcgccaat aacttcgcct tcgcaatggg ggcgctcttc 1920
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<210> 117
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 6x His tag

<400> 117
His His His His His His
  1   5

<210> 118
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 118
cgctcttttg cgcctcc   17

<210> 119
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 119
ccgccgattg cctgacc   17

<210> 120
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 120
gggttgcgct cgttg   15